

SEQUENCE LISTING

<110> JCR Pharmaceuticals Co., Ltd.

5 <120> Anti-HIV agents

<130> GP47

<160> 5

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<210> 1

<211> 1296

<212> DNA

<213> Homo sapience

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<400> 1

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20

gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tgc aac tgt gac 96

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp

20 25 30

25

tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att 144

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile

35 40 45

30

cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata 192

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile

50 55 60

gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga 240

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly

100544-0001

	65	70	75	80	
	aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct				288
	Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser				
5		85	90	95	
	gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt				336
	Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu				
		100	105	110	
10					
	cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg				384
	Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg				
		115	120	125	
15					
	agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa				432
	Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln				
		130	135	140	
	gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct				480
20	Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro				
		145	150	155	160
	cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc				528
	Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg				
25		165	170	175	
	ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg				576
	Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp				
		180	185	190	
30					
	ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg				624
	Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val				
		195	200	205	

	tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac	672
	Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His	
	210 215 220	
5	tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt	720
	Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly	
	225 230 235 240	
	cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg	768
10	Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val	
	245 250 255	
	gaa aac cta atc cta cac aag gac tac agc gct gac acg ctt gct cac	816
15	Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His	
	260 265 270	
	cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt	864
	His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys	
	275 280 285	
20	gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc teg atg tat	912
	Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr	
	290 295 300	
25	aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa	960
	Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys	
	305 310 315 320	
	gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt	1008
30	Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val	
	325 330 335	
	gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc	1056
	Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly	

10076434.034996

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	Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys			
5	355	360	365	
	aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc			1152
	Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu			
	370	375	380	
10	caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt			1200
	Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys			
	385	390	395	400
15	gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta			1248
	Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu			
	405	410	415	
	ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc tga			1296
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	Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp			
	20	25	30	

000421 000421

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35 40 45

5 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50 55 60

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65 70 75 80

10 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
85 90 95

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
100 105 110

15 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
115 120 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
20 130 135 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145 150 155 160

25 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
165 170 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
180 185 190

30 Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His

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	210	215	220
	Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly		
	225	230	235 240
5	Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val		
	245	250	255
	Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His		
10	260	265	270
	His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys		
	275	280	285
15	Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr		
	290	295	300
	Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys		
	305	310	315 320
20	Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val		
	325	330	335
	Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly		
25	340	345	350
	Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys		
	355	360	365
30	Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu		
	370	375	380
	Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys		
	385	390	395 400

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Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
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5 Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
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Lys Lys Phe Gly

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